

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2003, 02:22:59 ; Search time 9025 Seconds

(without alignments)  
11689.493 Million cell updates/sec

Title: US-09-804-472-1

Perfect score: 3625  
Sequence: 1 gaaccagctgcttcacgca.....aaaaaaaaaaaaaaaaaaaaa 3625

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

1: gb.ba:\*  
2: gb.htg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vl:\*  
15: em.ba:\*  
16: em.fun:\*  
17: em.hum:\*  
18: em.in:\*  
19: em.mu:\*  
20: em.om:\*  
21: em.or:\*  
22: em.ov:\*  
23: em.pat:\*  
24: em.ph:\*  
25: em.pl:\*  
26: em.ro:\*  
27: em.sts:\*  
28: em.un:\*  
29: em.vl:\*  
30: em.htg.hum:\*  
31: em.htg.inv:\*  
32: em.htg.other:\*  
33: em.htg.mus:\*  
34: em.htg.pln:\*  
35: em.htg.rod:\*  
36: em.htg.mam:\*  
37: em.htg.vrt:\*  
38: em.sy:\*  
39: em.htgo.hum:\*  
40: em.htgo.mus:\*  
41: em.htgo.other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3162.8	87.2	3953	9	HSCICN3	X78520 H. sapiens
2	2298	63.4	2457	9	AF029346	AF029346 Homo sapi
3	2294.8	63.3	2457	9	AF172729	AF172729 Homo sapi
4	2107.6	58.1	2457	4	AF029348	AF029348 Oryctolag
5	2104.8	58.1	2880	10	RATCIC3	D17521 Rat mRNA fo
6	2096.8	57.8	2758	10	MMICLN3	X78874 M.musculus
7	2095.4	57.8	2305	10	CPU83464	U83464 Cavia porce
8	2084.6	57.5	2283	10	AF133214	AF133214 Cavia por
9	2034.2	56.1	2659	10	AF142778	AF142778 Rattus no
10	2029.2	56.0	2457	10	AF029347	AF029347 Mus muscu
11	1632.2	45.0	2586	5	XICIC3	Y09941 Xenopus lae
12	1313.6	36.2	4538	5	AF182215	AF182215 Tilapia m
13	1202.6	33.2	2244	10	RNCCHAMP	Z36944 R.norvegicu
14	1188.6	32.8	3173	9	HSCICN5GN	X91906 H.sapiens v
15	1187	32.7	3046	9	AK056560	AK056560 Homo sapi
16	1178.6	32.5	2241	4	AF195523	AF195523 Oryctolag
17	1174.6	32.4	3353	9	AK092049	AK092049 Homo sapi
18	1172.6	32.3	2550	10	RATCIC5	D50497 Rattus norv
19	1169.4	32.3	2550	10	RNCIC5	Z56277 R.norvegicu
20	1164.6	32.1	2655	10	AF134117	AF134117 Mus muscu
21	1161.8	32.0	4454	9	AB019432	AB019432 Homo sapi
22	1156.2	31.9	2293	10	AF170492	AF170492 Homo sapi
23	1155.8	31.9	2739	10	AF326968	AF326968 Cavia por
24	1155.8	31.9	2739	10	MMICLN4MR	Z49916 M.musculus
25	1155.4	31.9	3214	5	HSCICPX	X77197 H.sapiens m
26	1141.2	31.5	2822	5	AF063904	AF063904 Xenopus l
27	1138	30.6	3016	5	XICIC5	Y09940 X.laeyis mr
28	1132.6	30.0	2306	4	AF274055	AF274055 Sus scrof
29	1088.8	30.0	135342	9	AC106878	AC106878 Homo sapi
30	1057	-29.2	3764	5	AF182216	AF182216 Tilapia m
31	1018	28.1	2447	10	BC005553	BC005553 Mus muscu
32	796	22.0	3318	3	AY129438	AY129438 Drosophila
33	789.6	21.8	3366	6	AX155079	AX155079 Sequence
34	718	19.8	726	9	H0M2D78B11	AF086418 Homo sapi
35	520.4	14.4	2686	3	AB035090	AB035090 Caenorhab
36	510.8	14.1	2705	3	AF173174	AF173174 Caenorhab
37	505	13.9	929	10	AF133215	AF133215 Cavia por
38	499.6	13.8	12745	10	AF347681S5	AF347684 Mus muscu
39	492.4	13.6	3600	10	AF347681S9	AF347688 Mus muscu
40	483.4	13.3	155872	2	AC097042	AC097042 Rattus no
41	478.6	13.2	73885	2	AC025307	AC025307 Homo sapi
42	478.6	13.2	150489	2	AC069491	AC069491 Homo sapi
43	478.6	13.2	157574	9	AL592293	AL592293 Human DNA
44	443.8	12.2	1424	9	HSDDCG	X81836 H.sapiens m
45	404.6	11.2	59865	2	AC014422	AC014422 Drosophila

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
HSCICN3	HSCICN3	H. sapiens RNA for CLCN3.	3953 bp	mRNA	linear	PR1 21-NOV-1995				
X78520.1	X78520	GI:854101								
Chloride channel; chloride channel 3; chloride channel protein;										
CLIC3 gene.										
Homo sapiens										
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;										
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.										
Borsani,G., Rugaili,E.I., Tagliatalela,M., Wong,C. and Ballabio,A.										
Characterization of a human and murine gene (CLCN3) sharing										

Pred. No. is the number of results predicted by chance to have a

similarities to voltage-gated chloride channels and to a yeast integral membrane protein  
Genomics 27 (1), 131-141 (1995)

JOURNAL MEDLINE 95394449

PUBMED 7665160

REFERENCE 2 (bases 1 to 3953)

AUTHORS Borsani, G.

TITLE Direct Submission

JOURNAL Submitted (29-MAR-1994) G. Borsani, Baylor College of Medicine, Institute for Molecular Genetics, One Baylor Plaza, Houston, TX 77030, USA

BASE COUNT	1111 a	766 c	940 g	1136 t	.
ORIGIN					
Query Match		87.2%	Score 3162.8;	DB 9;	Length 3953;
Best Local Similarity		98.0%;	Pred. NO. 0;		
Matches 3252; Conservative		0;	Mismatches 47;	Indels 21;	Gaps 4;

QY	237	GGACCTCATTTTACAATGACAAAATGGGAGGAGCATTTAAACAGTTCTACACATTTACTGGAT	296
Db	648	GGAACTCATTTTACAATGACAAAATGGGAGGAGCATTTTACAGTTCTACACATTTACTGGAT	707
QY	297	CTTTTGATGTGAACCAATTTCCAGGTGTTGTGTACATATGATGATTTTCCATCTACTATTGATTGG	356
Db	708	CTTTTGATGTGAACCAATTTCCAGGTGTTGTGTACATATGATGATTTTCCATCTACTATTGATTGG	767
QY	357	GTGCGAGAAAAATGTAAAGCAGAGATAGCGATAGACGATTCACACGCAAAAAAGAAAGCA	416
Db	768	GTGCGAGAAAAATGTAAAGCAGAGAAAGGCATAGACGGTATCAACAGCAAAAAAGAAAGCA	827
QY	417	TCAGCATGSGAAATGACAAAAAGTTTATATGATGCGGCGGTACAGATGGCTAGTAGTAACA	476
Db	828	TCAGCATGSGAAATGACAAAAAGTTTATATGATGCGGCGGTACAGATGGCTAGTAGTAACA	887
QY	477	CTAACGAGATTGGCATCAGGGGCACTGGCCGGATTAAATAGACATTTGCTCCGATTGGATG	536
Db	888	CTAACGAGATTGGCATCAGGGGCACTGGCCGGATTAAATAGACATTTGCTCCGATTGGATG	947
QY	537	ACTGACCTTAAGAGAGGCAATTTGCTTATGTGCTTGTGGTACACACCAGACAGATGCTGT	596
Db	948	ACTGACCTTAAGAGAGGCAATTTGCTTATGTGCTTGTGGTACACACCAGACAGATGCTGT	1007
QY	597	TGGGATGCTAATGAAACACACTTTGGAAGAGAGGATTAATATGTCACAGTGGAAAAATG	656
Db	1008	TGGGATGCTAATGAAACACACTTTGGAAGAGAGGATTAATATGTCACAGTGGAAAAATG	1067
QY	657	GCAGAAATTAAATCATAGGTCTCAAGCAGAGAGGCTCTGGTCTTATATCATGTGAACATATAATG	716
Db	1068	GCAGAAATTAAATCATAGGTCTCAAGCAGAGAGGCTCTGGTCTTATATCATGTGAACATATAATG	1127
QY	717	TACATCTTCTGGGCTTGAGTTTGGCTTCTTCTGCAAGTTTCCCTGGTAAAGATATTGGT	776
Db	1128	TACATCTTCTGGGCTTGAGTTTGGCTTCTTCTGCAAGTTTCCCTGGTAAAGATATTGGT	1187
QY	777	CCATATGCGCTGTGCTCTGCAATTCAGAGATTTAAACATATTTTAAAGTAGCATTCATCATC	836
Db	1188	CCATATGCGCTGTGCTCTGCAATTCAGAGATTTAAACATATTTTAAAGTAGCATTCATCATC	1247
QY	837	AGAGGTTACTTGGGAAAAATGACTTTTAAATGATTAAACCATCATTAAGTCTCGGCTGTG	896
Db	1248	AGAGGTTACTTGGGAAAAATGACTTTTAAATGATTAAACCATCATTAAGTCTCGGCTGTG	1307
QY	897	GCATCAGGTTTGAGTTTAGGAAAAAGAGTCCCTGGTACATCTCCGCTGGTGGCGGA	956
Db	1308	GCATCAGGTTTGAGTTTAGGAAAAAGAGTCCCTGGTACATCTCCGCTGGTGGCGGA	1367
QY	957	AATATCTTTTCCATCCTCTTTCACAAATATATAGCAACAAGACGCTAAAAAAAAGGAGGTG	1018
Db	1368	AATATCTTTTCCATCCTCTTTCACAAATATATAGCAACAAGACGCTAAAAAAAAGGAGGTG	1427
QY	1017	CTATCAGCTGCTCAGCTGCAGGGGTTCTGTAGCTTTTGTGTGCACCAATTTGGAGAGCTT	1076
Db	1428	CTATCAGCTGCTCAGCTGCAGGGGTTCTGTAGCTTTTGTGTGCACCAATTTGGAGAGCTT	1487
QY	1077	CTTTTACCCTGGAAAGAGGTAGCTATTAATTTTCTCTCAAACTTTATGAGAGATCAATT	1138
Db	1488	CTTTTACCCTGGAAAGAGGTAGCTATTAATTTTCTCTCAAACTTTATGAGAGATCAATT	1547
QY	1137	TTTGTGTGTATAGGCGCTGTGATTTGTTTGTAGTTCATCAATCATTTTGTAAACAGCGCT	1198
Db	1548	TTTGTGTGTATAGGCGCTGTGATTTGTTTGTAGTTCATCAATCATTTTGTAAACAGCGCT	1607
QY	1197	CTGCTCCTTTTTTATGAGGATATCATATACACATGCTATTTTGAACCTGTTTCTCTTTT	1256
Db	1608	CTGCTCCTTTTTTATGAGGATATCATATACACATGCTATTTTGAACCTGTTTCTCTTTT	1667
QY	1257	ATTCTTCTAGGGGATTTTGAAGGCTTTTGGGAGGCTTTTTCATTAAGGCAAAATATTTGCC	1316
Db	1668	ATTCTTCTAGGGGATTTTGAAGGCTTTTGGGAGGCTTTTTCATTAAGGCAAAATATTTGCC	1727

Oy	1317	TGSGTGTGAGCGCAAGTCCAGCAATTTGGAAATACCCGTTCTGGAAGTCATTATT	1376
Db	1728	TGGTGTGTGAGCGCAAGTCCAGCAATTTGGAAATACCCGTTCTGGAAGTCATTATT	1787
Oy	1377	GTTCACACCATTTACTGCTGTGATAGACCTTCCATAATCCATACATAGGCTAAACACAGT	1436
Db	1788	GTTCACACCATTTACTGCTGTGATAGACCTTCCATAATCCATACATAGGCTAAACACAGT	1847
Oy	1437	GAACGTATCAAAAGCTTTTTTACAGACGTGTGCTCCCTGGAAATCCCTCTCTTGTGTAC	1496
Db	1848	GAACGTATCAAAAGCTTTTTTACAGACGTGTGCTCCCTGGAAATCCCTCTCTTGTGTAC	1907
Oy	1497	TACGAAATGACATGAAATGCGCAATTAATTTGTGATGACATTCCTGATGTGCACAGC	1556
Db	1908	TACGAAATGACATGAAATGCGCAATTAATTTGTGATGACATTCCTGATGTGCACAGC	1967
Oy	1557	ATTGAGATATTTCAGCTATATATGGAGATTATGTGCTGTGCACATATTAAATCATATATG	1616
Db	1968	ATTGAGATATTTCAGCTATATATGGAGATTATGTGCTGTGCACATATTAAATCATATATG	2027
Oy	1617	ACAGTATTCACTTTTGGCATCAAGTGTTCATCAGAGCTTTTCATCCCGAGATGGCAATT	1676
Db	2028	ACAGTATTCACTTTTGGCATCAAGTGTTCATCAGAGCTTTTCATCCCGAGATGGCAATT	2087
Oy	1677	GGAGCATCCGAGAGAGATTTGGGGGATTCGGGTGTGAGACAGCTTGCTACTATACCAC	1736
Db	2088	GGAGCATCCGAGAGAGATTTGGGGGATTCGGGTGTGAGACAGCTTGCTACTATACCAC	2147
Oy	1737	GACGTGTTTATCTTTAAGGAGTGTGTGAGGTGTGGGGGCGATTTGATACACGTGGCCTT	1796
Db	2148	GACGTGTTTATCTTTAAGGAGTGTGTGAGGTGTGGGGGCGATTTGATACACGTGGCCTT	2207
Oy	1797	TATCCCATGTTGTGCTGCTGCTGATCCTTAAGGTGTGTGACAAAGATACGTCTCCCTG	1856
Db	2208	TATCCCATGTTGTGCTGCTGCTGATCCTTAAGGTGTGTGACAAAGATACGTCTCCCTG	2267
Oy	1857	GTGCTTATGTTTTTGAGCTTACTGAGAGCTTGGAAATATTTGTTCCCTTATGGCTGCA	1916
Db	2268	GTGCTTATGTTTTTGAGCTTACTGAGAGCTTGGAAATATTTGTTCCCTTATGGCTGCA	2327
Oy	1917	GTCATGACCATTAATGGGTGTGAGATGGCTTTGGCAGGAGGACATTTATGAAGCACAC	1976
Db	2328	GTCATGACCATTAATGGGTGTGAGATGGCTTTGGCAGGAGGACATTTATGAAGCACAC	2387
Oy	1977	ATCCGATTTAATGGATACCTTCTTCTTGATATGCAAAAGAA-----GAATTCATCATATCC	2030
Db	2388	ATCCGATTTAATGGATATACCTTCTTCTTGATATGCAAAAGAAATTTGCAATTCATCATATCC	2447
Oy	2031	ACCTGTGCTGTGACGTTATGAGACCTCGAAGGAATGATCTCCCTTAGCTGTCTGTGCA	2090
Db	2448	ACCTGTGCTGTGACGTTATGAGACCTCGAAGGAATGATCTCCCTTAGCTGTCTGTGCA	2507
Oy	2091	CAGACCAATATGACATGTGATATATGAAGAACATGATTAATGAAGAACAGCTACTACATGGA	2150
Db	2508	CAGACCAATATGACATGTGATATATGAAGAACATGATTAATGAAGAACAGCTACTACATGGA	2567
Oy	2151	TTTCTCTCATTAATGTCAAAAGAAATCTCAGAGATTAGTGGATTTTGCCCTCAGAAAGAC	2210
Db	2568	TTTCTCTCATTAATGTCAAAAGAAATCTCAGAGATTAGTGGATTTTGCCCTCAGAAAGAC	2627
Oy	2211	CTGACCAATGCAATAGAAAGTGGCAGGAAAAAACAGAAAGATATGTTGGAGTTCTGCG	2270
Db	2628	CTGACCAATGCAATAGAAAGTGGCAGGAAAAAACAGAAAGATATGTTGGAGTTCTGCG	2687
Oy	2271	GTGTGTTTTGACAGCACACCCCATCTCTTCCAGCAGAAAGTCTGTGGCCATTGAAGTT	2330
Db	2688	GTGTGTTTTGACAGCACACCCCATCTCTTCCAGCAGAAAGTCTGTGGCCATTGAAGTT	2747
Oy	2331	CGAAGCATTTCTGACATGAGACCTTTTACAGTGTGACAGCACACCCCATGAGATTTGTG	2390
Db	2748	CGAAGCATTTCTGACATGAGACCTTTTACAGTGTGACAGCACACCCCATGAGATTTGTG	2807
Oy	2391	GTGATATATTTCCGAAAGCTGGGACGTGAGGACATGAGCTTTGTATACATCACAATGGGCGCTC	2450

[illegible]

[illegible]

QY	477	CTACAGGATTTGGCATAGGGGACAGCGGCGGATTTAAATGACATTTGCTGGCATTTGGATG	536
Db	400	CTAACAGGATTTGGCATATAGGGGCACTGGCGGATTTAATGACATTTGCTGGCATTTGGATG	459
QY	537	ACTACGCTAAAGGAGGGCACTTTGGCTTTAGTGGCTTTGGCTAGACACGACGACGTCGT	596
Db	460	ACTGACCTAAAGGAGGGCACTTTGGCTTTAGTGGCTTTGGCTAGACACGACGACGTCGT	519
QY	597	TGGGGATCTAATGAACACATTTGGAAGAGGAGTAAATGTCCACAGTGGGAAACATGG	656
Db	520	TGGGGATCTAATGAACACATTTGGAAGAGGAGTAAATGTCCACAGTGGGAAACATGG	579
QY	657	GCAGATTTAATCAATAGGTCAAGACAGAGGGGCGGCTTTATATCATGTAACATCAATAG	716
Db	580	GCAGATTTAATCAATAGGTCAAGACAGAGGGGCGGCTTTATATCATGTAACATCAATAG	639
QY	717	TACATCTTGGGGCTTGAATTTGGCTTTTGGCATTTTCCGTGGTAAAGGATTTTGGT	776
Db	640	TACATCTTGGGGCTTGAATTTGGCTTTTGGCATTTTCCGTGGTAAAGGATTTTGGT	699
QY	777	CCATATGCGCTGTGGCTGTGGAATTTCCAGAGATTTAAACATTTTAAATGATTCATCATC	836
Db	700	CCATATGCGCTGTGGCTGTGGAATTTCCAGAGATTTAAACATTTTAAATGATTCATCATC	759
QY	837	AGAGGTTACTTGGGAAATATGACCTTTAAATGATTTAAACATCAATATGCTGGCTGTG	896
Db	760	AGAGGTTACTTGGGAAATATGACCTTTAAATGATTTAAACATCAATATGCTGGCTGTG	819
QY	897	GCATCAGGTTTGAATTTAGGAAAAAGAGTCCCGTGTCATGTTGCCGTGTCTGCGGA	956
Db	820	GCATCAGGTTTGAATTTAGGAAAAAGAGTCCCGTGTCATGTTGCCGTGTCTGCGGA	879
QY	957	AATATCTTTTCTTACCTCTTTCCAAAGTATACGACAAACGAAGCTTAAAAAGGAGGTG	1016
Db	880	AATATCTTTTCTTACCTCTTTCCAAAGTATACGACAAACGAAGCTTAAAAAGGAGGTG	939
QY	1017	CTATACAGCTCCACAGCTGCAGGGGTTTGTAGAGCTTTTGGTGACACAAATTTGGAGAGTT	1076
Db	940	CTATACAGCTCCACAGCTGCAGGGGTTTGTAGAGCTTTTGGTGACACAAATTTGGAGAGTT	999
QY	1077	CTTTTATAGCCTGGAAGAGTTACCTATATTTTCTCTCAAAACTTTTATGAGATCATTT	1136
Db	1000	CTTTTATAGCCTGGAAGAGTTACCTATATTTTCTCTCAAAACTTTTATGAGATCATTT	1059
QY	1137	TTTGTCTCTTAAAGGCGTGCAATTTGTTTGAAGTCCATCAATTCATTTGGTAAACGCCGT	1196
Db	1060	TTTGTCTCTTAAAGGCGTGCAATTTGTTTGAAGTCCATCAATTCATTTGGTAAACGCCGT	1119
QY	1197	CTGTGCTTTTTTATGTGAGTATTCATATACCATGATGTAACCTTTTGAAGCTGTTTCTTTT	1256
Db	1120	CTGTGCTTTTTTATGTGAGTATTCATATACCATGATGTAACCTTTTGAAGCTGTTTCTTTT	1179
QY	1257	ATTTCTTTACGGGATTTTGGAGGGCTTTTGGGAGCCTTTTATTTAGGGCAAAATATTTCC	1316
Db	1180	ATTTCTTTACGGGATTTTGGAGGGCTTTTGGGAGCCTTTTATTTAGGGCAAAATATTTCC	1239
QY	1317	TGGTGTGTGACAGCAAGTCCAGAAATTTGGAAGATATCCGCTGTGGAAGTCAATTT	1376
Db	1240	TGGTGTGTGACAGCAAGTCCAGAAATTTGGAAGATATCCGCTGTGGAAGTCAATTT	1299
QY	1377	GTTCGACCACTTACTGCTGTGATAGCCTTCCCTAAATTCATACACTAGGCTTAAACACAGT	1436
Db	1300	GTTCGACCACTTACTGCTGTGATAGCCTTCCCTAAATTCATACACTAGGCTTAAACACAGT	1359
QY	1437	GAACTGATCAAAAGACTTTTACAGACTGTGGTCCCGTGGAAATCCTTTCTTTTGTGAC	1486
Db	1360	GAACTGATCAAAAGACTTTTACAGACTGTGGTCCCGTGGAAATCCTTTCTTTTGTGAC	1419
QY	1497	TACGGAATATACATGATGCACTAAATTTGTTCGATGCAATTCGATGCTGCACAGCAGC	1556
Db	1420	TACGGAATATACATGATGCACTAAATTTGTTCGATGCAATTCGATGCTGCACAGCAGC	1479

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OY 1557 ATGAGTAAATTCAGCTAATATGACGATTATGCTGGCACTCATATTTAAATCATATG 1616
    |||||||
Db 1480 ATTGAGTAATATTCAGTAATATGACGATTATGCTGGCACTCATATTTAAATCATATG 1539
OY 1617 ACATATTCACCTTTGGCATCAAGCTTCATCAGGCTTTGTCATCCCGAGATGGCATT 1676
    |||||||
Db 1540 ACATATTCACCTTTGGCATCAAGCTTCATCAGGCTTTGTCATCCCGAGATGGCATT 1599
OY 1677 GGAGCATGCGAGAGAGATTTGGGGATTGGGTGGAGCAGCTTGGCTACTATCACCAC 1736
    |||||||
Db 1600 GGAGCATGCGAGAGAGATTTGGGGATTGGGTGGAGCAGCTTGGCTACTATCACCAC 1659
OY 1737 GACTGGTTATCTTTAAAGAGATGGTGTGAGGTCGGGGCTGATTCATACCTGGCCTT 1796
    |||||||
Db 1660 GACTGGTTATCTTTAAAGAGATGGTGTGAGGTCGGGGCTGATTCATACCTGGCCTT 1719
OY 1797 TATCCCATGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1856
    |||||||
Db 1720 TATCCCATGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1779
OY 1857 GTGGTTATGTTTGTGAGCTTACTGAGAGCTTGGATATATTTGTTCCCTTATGGCTGA 1916
    |||||||
Db 1780 GTGGTTATGTTTGTGAGCTTACTGAGAGCTTGGATATATTTGTTCCCTTATGGCTGA 1839
OY 1917 GTCATGACCACTAAATGGGTTGAGATGCCCTTGGCAGGAGCATTTATGAACACAC 1976
    |||||||
Db 1840 GTCATGACCACTAAATGGGTTGAGATGCCCTTGGCAGGAGCATTTATGAACACAC 1899
OY 1977 ATCCGATTAATGATATCCCTTTTGTGATGCAAAAGAAATTCATCATACCCCTG 2036
    |||||||
Db 1900 ATCCGATTAATGATATCCCTTTTGTGATGCAAAAGAAATTCATCATACCCCTG 1959
OY 2037 GCTGCTACGCTTATGAGACCTCGAAGAAATGATCCTCCCTAGCTGCTGACACAGAC 2096
    |||||||
Db 1960 GCTGCTACGCTTATGAGACCTCGAAGAAATGATCCTCCCTAGCTGCTGACACAGAC 2019
OY 2097 AATATGACAGTGATATATGAAACATGATTAATGAACCAAGCTCAATGATTTCT 2156
    |||||||
Db 2020 AATATGACAGTGATATATGAAACATGATTAATGAACCAAGCTCAATGATTTCT 2079
OY 2157 GTCATATGTCAAAAGAAATCGAGATTTAGTGGATTGGCCCTCAGAAAGACTTGACA 2216
    |||||||
Db 2080 GTCATATGTCAAAAGAAATCGAGATTTAGTGGATTGGCCCTCAGAAAGACTTGACA 2139
OY 2217 ATTGCAATAGAAAGTGCAGAGAAAAACAAGAAATGATCGTTGGCAGCTTCCGGGTGT 2276
    |||||||
Db 2140 ATTGCAATAGAAAGTGCAGAGAAAAACAAGAAATGATCGTTGGCAGCTTCCGGGTGT 2199
OY 2277 TTGTCACAGACACCCCATCTCTTCCAGCAGAAAGTCCCTGGCCATTGAAGCTTGAAGC 2336
    |||||||
Db 2200 TTGTCACAGACACCCCATCTCTTCCAGCAGAAAGTCCCTGGCCATTGAAGCTTGAAGC 2259
OY 2337 ATTCCTGACATGAGCCCTTTTACAGTGACAGACCAACCCCAATGAGATTGGTGGAT 2396
    |||||||
Db 2260 ATTCCTGACATGAGCCCTTTTACAGTGACAGACCAACCCCAATGAGATTGGTGGAT 2319
OY 2397 ATTTTCGGAAGCTGGGACTGAGGACATGCTTGTAACTACAATGAGGCGCTCTTGGC 2456
    |||||||
Db 2320 ATTTTCGGAAGCTGGGACTGAGGACATGCTTGTAACTACAATGAGGCGCTCTTGGC 2379
OY 2457 ATTATTAACAAAAAAGATATCTCCGCGATATGCGCCAGACGGAACCAAGACCCCGCT 2516
    |||||||
Db 2380 ATTATTAACAAAAAAGATATCTCCGCGATATGCGCCAGACGGAACCAAGACCCCGCT 2439
OY 2517 TCATATATGTTCACTGA 2534
    |||||||
Db 2440 TCATATATGTTCACTGA 2457
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RESULT 3
AF172729 AF172729 2457 bp mRNA linear PRI 05-JUN-2001
LOCUS DEFINITION Homo sapiens chloride channel 3 mRNA, complete cds.

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ACCESSION AF172729
VERSION AF172729.1 GI:5759223
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
REFERENCE
AUTHORS Huang,P., Liu,J., Di,A., Robinson,N.C., Musch,M.W., Kaezel,M.A.
and Nelson,D.J.
TITLE Regulation of human CLC-3 channels by multifunctional
Ca2+/calmodulin-dependent protein kinase
JOURNAL J. Biol. Chem. 276 (23), 20093-20100 (2001)
MEDLINE 21282914
PUBMED 11274166
REFERENCE
AUTHORS 2 (bases 1 to 2457)
Huang,P., Di,A., Kaezel,M.A., Musch,M.W., Xie,W., Johnson,X.D. and
Nelson,D.J.
TITLE Molecular identification of human CLC-3 as the CAMKII-activated
chloride channel: A potential cyclic fibrosis bypass pathway
JOURNAL Unpublished
AUTHORS 3 (bases 1 to 2457)
Huang,P., Nissen,J., Johnson,X.D. and Nelson,D.J.
TITLE Direct Submission
JOURNAL Submitted (27-JUL-1999) Pharmacological & Physiological Sciences,
The University of Chicago, 947 E. 58th Street MC0926, Chicago, IL
60637, USA
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DEFINITION complete cds.
ACCESSION AF029348
VERSION AF029348.1 GI:2599551
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SOURCE Oryctolagus cuniculus.
ORGANISM Oryctolagus cuniculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorphia; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 2457)
AUTHORS Rae, J.L. and Shepard, A.R.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-1997) Physiology and Biophysics, Mayo Foundation,
200 1st Street SW, Rochester, MN 55905, USA
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 VERSION D17521.1 GI:473727  
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 AUTHORS Kawasaki, M., Uchida, S., Monkawa, T., Miyawaki, A., Mikoshiba, K., Marumo, F., and Sasaki, S.  
 TITLE Cloning and expression of a protein kinase C-regulated chloride channel abundantly expressed in rat brain neuronal cells  
 JOURNAL Neuron 12 (3), 597-604 (1994)  
 MEDLINE 94206538  
 REFERENCE 2 (bases 1 to 2880)  
 AUTHORS Kawasaki, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-AUG-1993) Masanobu Kawasaki, Tokyo Medical and Dental University, Second Department of Internal Medicine, 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111, Fax:03-3818-7177)  
 COMMENT Submitted (31-Aug-1993) to DDBJ by: Masanobu Kawasaki  
 Second Dept. of Internal Medicine  
 Tokyo Medical and Dental University  
 1-5-45 Yushima, Bunkyo-ku  
 Tokyo 113  
 Japan  
 Phone: 03-3813-6111  
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ACCESSION X78874.1 GI:854275  
VERSION chloride channel 3; Clcn3 gene.  
KEYWORDS Mus musculus.  
SOURCE Mus musculus.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2758)  
AUTHORS Borsani, G.  
TITLE Direct Submission  
JOURNAL Submitted (19-APR-1994) G. Borsani, Baylor College of Medicine, Institute for Molecular Genetics, One Baylor Plaza, Houston TX 77030, USA  
2 (bases 1 to 2758)  
AUTHORS Borsani, G., Rugaril, E. I., Tagliabue, M., Wong, C. and Ballabio, A.  
TITLE Characterization of a human and murine gene (CLCN3) sharing similarities to voltage-gated chloride channels and to a yeast integral membrane protein  
JOURNAL Genomics 27 (1), 131-141 (1995)  
MEDLINE 95394449  
PUBMED 7665160

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ACCESSION AF133214
VERSION AF133214.1 GI:4928465
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SOURCE Cavia porcellus.
ORGANISM Cavia porcellus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
REFERENCE 1 (bases 1 to 2283)
AUTHORS Varela,D., Cid,L.F. and Sepulveda,F.V.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-1999) Instituto de Ciencias Biomedicas, Facultad
de Medicina, Universidad de Chile, Independencia 1027, Santiago, RM
6530499, Chile
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Best Local Similarity 94.6%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
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 ORGANISM Rattus norvegicus.  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 REFERENCE 1 (bases 1 to 2659)  
 AUTHORS Shimada,K., Li,X., Xu,G., Nowak,D.E., Showalter,L.A. and Weisman,S.A.  
 TITLE Expression and canalicular localization of two isoforms of the ClC-3 chloride channel from rat hepatocytes  
 JOURNAL Am. J. Physiol. Gastrointest. Liver Physiol. 279 (2), G268-G276 (2000)  
 MEDLINE 20378002  
 PUBMED 10915634  
 REFERENCE 2 (bases 1 to 2659)  
 AUTHORS Shimada,K., Nowak,D.E. and Weisman,S.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-APR-1999) Physiology and Biophysics, University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555-0641, USA  
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VERSION	AF029347.1	GI:2599549						
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AUTHORS	1 (bases 1 to 2457)							
TITLE	Rae, J.L. and Shepard, A.R.							
JOURNAL	Submitted (09-OCT-1997) Physiology and Biophysics, Mayo Foundation, 200 1st Street SW, Rochester, MN 55905, USA							
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Db	460	ACTGACCTGAAGGAGGGCATCTGCTCAGTGTGATTTGGTACACACATTAAGACAGTGTGT	519		
Oy	557	TGGGATCTAATGAACAACATTTGAAGAGAGGGATTAATGTCCACAGTGGAAACATG	656		
Db	520	TGGGGCTCTAATGAGCAACGTTTGAAGAGGGATTAATGTCCACAGTGGAAACATG	579		
Oy	657	GCAGATTAATCATAGTCTCAGCAGAGAGGGTCCGTCTTATATCATGTAACATCATTAATG	716		
Db	580	GCAGATTAATCATTTGSCCAAGCAGAGGGCCCTGGATCTTATATCATGTAACATCATTAATG	639		
Oy	717	TACATCTTCTGGGCCCTTGAATTTGGCTTTCTGTGACGTTTCCCTGTGAAGGATTTTCT	776		
Db	640	TATATCTTTTGGCTTGAATTTGGCTTTCTGTGACGTTTCCCTGTGAAGGATTTTCT	699		
Oy	777	CCATATGCCCTGGCTGTGGAATTCACAGAGATTAACATTTTAAGTGGATTCATCATC	836		
Db	700	CCATATGCCCTGGCTGTGGAATTCACAGAGATTAACATTTTAAGTGGATTTATCATC	759		
Oy	837	AGAGGTTACTTGGGAAAAATGACCTTTTAATGATTTAAACCATCACATTTAGTCTGGCTGTG	896		
Db	760	AGAGGATTACTTGGGAAAAATGACCTTTTAATGATTTAAACATCATCAGTTAGTCTGGCTGTG	819		
Oy	897	GCATCAGGTTTGAATTTAGSAAAAAGAGTCCCTGTGTACATGTTGCTGTGCTGGCGA	956		
Db	820	GCATCAGGTTTGAATTTAGSAAAAAGAGTCCCTGTGTACATGTTGCTGTGCTGTGGA	879		
Oy	957	AATATCTTTTCTCCCTCTTCCAAAGATATAGCACAAAGAGCATTAATAAAAAAGGAGGTG	1016		
Db	880	AATATCTTTTCTCCCTCTTCCAAAGATATAGCACCAATGAAGCATTAATAAAAAAGGAGGTG	939		
Oy	1017	CTATACGCTGCTACGCTGACGAGGGTTTCTGTAGCTTTTGTGTGACACCAATTTGACGAGATT	1076		
Db	1000	CTTTTGAAGCTTGGAGAGGTTTACATTAATTTTCCCTCAAAACCTTTATGAGGATCATTT	1058		
Oy	1137	TTTGCTGCTTTAGTGGCTGCATTTGTTTTGAGGTCCATCAATCCATTTTGTAAACGCCGT	1196		
Db	1060	TTTGCTGCTTTAGTGGGAGCATTTGTGTTTTGAGATTCATCAATCCATTTGTAAACGCCGT	1119		
Oy	1197	CTGCTCTTTTATATGTGAGATATCATATACACATGTATCTTTTGAACGTGTTCTCTTTT	1256		
Db	1120	CTGCTCTCTTTTATATGTGAGATATCATATACACATGTATCTTTTGAACGTGTTCTCTTTT	1179		

QY	1257	ATTTCCTAGGGGATTTGGAGGCTTTGGGGAGCCTTTTCAATGAGGCAAAATATGGC	1316
Db	1180	ATTTCCTAGGGGATTTGGAGGCTTTGGGGAGCCTTTTCAATGAGGCAAAATATGGC	1239
QY	1317	TGCTGCTGCAGCGCAAGTCCACGAAATTTGGAAAGATATCCGTTCTGGAGTCATATY	1376
Db	1240	TGCTGCTGCAGCGCAAGTCCACGAAATTTGGAAAGATATCCGTTCTGGAGTCATATY	1299
QY	1377	GTTGCGACCACTTACCTGCTGTGATAGGCTTCCCTAATCCATACACTAGGCTTAACACAGT	1436
Db	1300	GTTGCGACCACTTACCTGCTGTGATAGGCTTCCCTAATCCATACACTAGGCTTAACACAGT	1359
QY	1437	GAACGTATCAAAAGAGCTTTTACAGACTGTGGTCCCTGGATATCCTCTCTTTGTGTAC	1496
Db	1360	GAACGTATTAAGAGCGCTTTACAGATGTGGGCGCTGGATATCCTCTCTCTGTGTAC	1419
QY	1497	TACAGAAATACACTGAATGCCAGTAAATTTGCATGACATTTCTGATCTCCACAGGC	1566
Db	1420	TACAGAAATACACTGAATGCCAGTAAATTTGTTCAGATATCTCCAGCGCTCCAGCAGGC	1479
QY	1557	ATTGAGCATATATTCAGCTATATGAGCGATATGCGTGGACCTCATTTTAAATCATATATG	1616
Db	1480	GTTGAGCATATATTCAGCTATCTGGCAGTTGTGCTTACGCGCTCATATTTAAATATATATG	1539
QY	1617	ACAGTATTCACCTTTGGCATCAAGGTTTCCATCAGGCTTTTCATCCCGAGATGGCATY	1676
Db	1540	ACAGTATTCACCTTTGGTATCAAGGTTCCCGTCAGGCTTTTATCCCGAGATGGCATY	1599
QY	1677	GGAGCGATCCAGGAAGATTTGGGGGATTTGCGGTGAGGACGCTTCCCTATATCACAC	1736
Db	1600	GGAGCGCATTCGAGGGAATTTGGGGGATTCGTGTGAGCACGCTTCCCTATATCACAC	1659
QY	1737	GACTGGTTATCTTTAAGGAGTGTGTGAGTGGGGCGATTTGCATTACACCTGGGCTY	1796
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QY	1797	TATGCCATGGTGGTCTGCTGCTGATGCTTAAAGTGTGTGACAAAGATGATGTCCTCTG	1856
Db	1720	TATGCCATGGTGGGCTGCTGCTGCTTAAAGTGTGTGACAAAGATGATGTCCTCTG	1779
QY	1857	GTTGGTTATTTTGTGAGCTTACCTGGAGGCTTGGAAATATTTGCCCTATGGGTCGA	1916
Db	1780	GTTGGTTATTTGTTTGACTTACTGAGGCTTGGAAATATTTGTTCCCTTATGGCTGCA	1839
QY	1917	GTCATGACCACTAAATGGGTGTGAGATGCCCTTGGCAGGGAAGGCAATTTATGAAGCAC	1976
Db	1840	GTAATGACCACTAAATGGGTGTGATGCCCTTGGTAAAGGAAGTATTTATGAAGCAC	1899
QY	1977	ATCCGATTAATGATATCCCTTTCTTGGATGCAAAAGAAGATTCATCATACACCTG	2036
Db	1900	ATCCGATTAATGGGATACCTTTCTTGGATGCAAAAGAAGATTCATCATACACCTG	1959
QY	2037	GCTGCTACGTTATWGAGCCTCGAAGATTTGATTCCTCCCTTAAGCTGTGCTACACAGAC	2096
Db	1960	GCTGCTATGTTATWGAGCCTCGAAGATTTGATTCCTCCCTTAAGCTGTGTTACACAGAC	2019
QY	2097	AATATGACAGTGAATATAGAAAACATGATTAATGAACACGCTACAAATGGAATTCCT	2156
Db	2020	AATATGACAGTGAATATGACATAGAAAACATGATTAATGAACACGCTAATATGGCTTCCT	2079
QY	2157	GTCATATATGCAAAAGATCTCAGAGATTTAGTGGGATTTGCCCTCAGAAGAGACTGACA	2216
Db	2080	GTCATATATGCAAAAGATCTCAGAGATTTAGTGGGATTTGCCCTCAGAAGAGACTGACT	2139
QY	2217	ATTGCAATAGAAAGTCCACAGAAAAACAAGAAAGTATGCTGTGACATTCGCGGGTGTG	2276
Db	2140	ATTGCAATAGAAAGTCCGAGAAAAACAAGAAAGATTTGTTGGCAGTTCTCGGGGTGTG	2199
QY	2277	TTTGGACAGACACCCCATCTCTCCAGCAGAAAGTCTCGGCCATTTGAGCTTTGAAGC	2336
Db	2200	TTTGGACAGATCTCATCTCTCTCCAGCAGAAAGTCTCCAGGCCATTTAAACTAGAGAGC	2259

Y	2337	ATTCCTGCATGAGCCCTTTTACATGACAGACACACCCCAAGGATGTTGGTGGAT	2396
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Db	2260	ATCCTTGACATGAGCCCTTTTACATGACAGACACACCCCAAGGATGTTGGTGGAT	2319
Y	2397	ATTTCCGAAGCTGGGAGCTGAGGACGTCCTTGTAACTCAAAATGGCGCCTCTTGGC	2456
Db	2320	ATCTTCCGAAGCTTGTCTGATGAGGACGTCCTTGTAACTCAAAAGGACGTCCTCTTGGC	2379
Y	2457	ATTATTAACAAAAAAGATATCTCTCGGATATGCGCCAGAGCGCAACACGACCCGCT	2516
Db	2360	ATTATTAACAAAAAAGATATCTCTCGGATATGCGCCAGAGCGCAACACGACCCGCT	2439
Y	2517	TCATATATGTTCAACTGA	2534
Db	2440	TCATATATGTTCAACTGA	2457
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AUTHORS	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
JOURNAL	Xenopodinae; Xenopus.		
AUTHORS	1 (bases 1 to 2586)		
JOURNAL	Lindenthal, S.M.B.		
AUTHORS	2 (bases 1 to 2586)		
JOURNAL	Lindenthal, S.M.B.		
AUTHORS	Submitted (04-DEC-1996) S.M.B. Lindenthal, Laboratoire Jean Meatz,		
JOURNAL	Physiologie Des Membranes, La Darse - B.P. 68, 06230		
REMARK	Villefranche-Sur-Mer, FRANCE		
REFERENCE	revised by [4]		
AUTHORS	3 (bases 1 to 2586)		
JOURNAL	Lindenthal, S.M.B.		
COMMENT	Submitted (22-DEC-1999) S.M.B. Lindenthal, CNRS/ERS 1253,		
FEATURES	Laboratoire Jean Meatz, BP 68, La Darse 06238, Villefranche s/m		
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ORIGIN

Query Match	45.0%;	Score 1632.2;	DB 5;	Length 2586;
Query Match	45.0%;	Score 1632.2;	DB 5;	Length 2586;

Matches 1953; Conservative 0; Mismatches 513; Indels 3; Gaps 1;

1

OY	159	ATGATCGCTTTCGACCCCTTAATTTGGCTTAAGACGGGGGAGAGACAATATTTCCCTG	218
Db	91	ATGGATATTCCTTCAGATCCCTACCTGCGCTTAATGATGAGGATGGAGACAAATATTCCTCTC	150
OY	219	AGGGAATTTACATAAAGAGAGAACTCATTTATACATGACAAATGAGGCGAGATTAAACGT	278
Db	151	CGGGATCTGCATAAAGAGAGACACATTTATCTGTCACAAAGTGAGGTGCATTTAAACGC	210
OY	279	TCTACATTTACAGATCTTTTGGATGTAACCAATTCACAGGTGGTGTGCATATATCATAT	338
Db	211	ACGAGTCACTATTTTGGATCTCTCTTAAGTGAACCATTCGCCAGGAGTGGGACCTATATATAC	270
OY	339	TTCCATCTATTTGATTTGGTGGGAGAAAATGTAAAGACAGAAAGCATAGACGATC	398
Db	271	TTTTCATACCTAGCTGGGGTGGGAAAAATGCAAGACAGAGACGACACAGCGGGATTA	330
OY	399	AACGCAAAAAGAAAGATATAGCATGGGAATCACAAAAGTTTGATGATCCGTGCGCA	458
Db	331	AACGCAAGAAAGAAAGAAATTCGATGGGAACTAAGCAAAAAGTCTGTACGATCCCTGCT	390
OY	459	GGATGGCTAGTAGTAACTAACAGGATTTGCCATCAGGGGCACTGCGCGGATTAATAGAC	518
Db	391	GGATGGCTGTACTCACACTAACCGGTTTAAAGCATCAGGTGCCCTTGACGGCTTTTATAC	450
OY	519	ATTGCTCCCATTTGGATGACCTAAAGAGAGGCAATTGGCTTAAGTCCGTTGGTGAAC	578
Db	451	ATTGCTCGACACTGATGAGGAGATTTTAAAGAAAGATTTTGTATGACCGCATTCCTGGTTT	510
OY	579	AACCAGACAGATGCTGTGGGATCTTAATGAACACATTTGAAGAGAGGATTAATGT	638
Db	511	AACCATTAACAGTGTGCTGGGACTCCAAAGAAAGCAACATTTGAAGAGAGAACAAAGTC	570
OY	639	CCACAGTGGAAAACATGGGAGAAATTAATCATAGCTCAAGAGAGGTCCTGGTCTTAT	698
Db	571	CTCTAGTGGCAGACATGGGCAACCTAATTAATTTGGCCAGCAAGAAAGTCTGTGATCTTAT	630
OY	699	ATCATGAACTACATATATGATCATCTTCTGGGCCCTTGAGTTTTCCTTCTGTGCAGTTTCC	758
Db	631	ATAATGAAATTAATTCATGATCAATTTTTTGGGCCCTTAAGTTTGGCCTTCTCCGCTGTGT	690
OY	759	CTGCTAAGGATTTTGGCTCATATAGCTGTGGCTGTGGAATTCAGAGATTTAAACTATTT	818
Db	691	CTTGCGAAATTAATTTGCCCTTATGCTTGTGTGTGATGGAATACAGAAATTTAAACTATTT	750
OY	819	TTAAGTGGATTCATCATCAGAGGTTACTTGGGAAAATGCACTTTAATGATTTAAACATTC	878
Db	751	TTAAGCGGAATTCATCAATCCGTGATACCTGGGAAAATGCACTTTAATGATTTAAACATTC	810
OY	879	ACATTAATCCGTGCGTGGCATCAGGTTTGAATTTGCAAAAAGAGTCCCTGGTATAT	938
Db	811	ACGTGGTCTTCTGCTGTGGGCTCAGGTTTAAGCTTAGGGAAGAAAGTCCCTTAATACAT	870
OY	939	GTTGCTGTGTGCTGCGGAATATCTTTTCCCTACCTCTTTCCAAAGTATAGCAACAAGAA	998
Db	871	GTTTCATAGCTGTGTGGCAACATATTTTCTCACTGTTCCTCCAAAGTACAGCACTAATGAG	930
OY	999	GCTAAAAAAGGGGAGGTCATACGCTGGCTCAGCTGCAGGGGTTTCTGTACCTTTTGGT	1058
Db	931	GCAAGAAAAAGAGAGGTTCTGTACAGCAATCAGCTGCTGTGTCTTCTGTGCTTTTGGCA	990
OY	1059	GCACCAATTTGGAGAGTCTTTTTTTAACTGGAAGAGGTTAGCTATATTTTCTCTCAAA	1118
Db	991	GCTCCCAATGAGTGGAGATCTTTTAACTGTGGAAGAGTGAAGTACTATTTTCCCTTAAAG	1050
OY	1119	ACTTTATGAGGATCATTTTGTGCTGTTAATGTGCTGCATTTGTTTGAAGTCCATCAAT	1178
Db	1051	ACATTTATGAGGATCATTTCTTGAGGCTTAATGACAGCAATTTGTTCTTAAGGCAATTTAAC	1110

QY	1179	CCCTTGGTAAAGCCGCTGCGCCCTTTTATATGAGATATCAATCAACGATGACTT	1238
Db	1111	CTTTTGGAAACAGCCCTCTTGCTCTTCTATATGATATATCAATCCCATGATTTGC	1170
QY	1239	TTTGAACTGTTCCCTTTATTTCTTCTAAGGGATATTTGGAGGCTTTGGGACCTTTTTC	1298
Db	1171	TTTGAACTATTCACATTTATTTCTTACTGGGATATTTGGAGACTTTGGGAGCCGTTTC	1230
QY	1289	ATTAGGCAATATTTGCTCTGTGCTGCAGCCAGTCCAGAAATTTTGGAAATATCC	1358
Db	1231	ATCCGTGCGAATATTTGCTGTGTCCCGGCGCCCAATCAACGATTTTGGAGGATATCCA	1290
QY	1359	GTTCGTGAATCATTTATTTGTTGAGCCATTACTGCTGTGATATGCTTCCCTCAATCCATATC	1418
Db	1291	GTAATGAGGTTATTCGCCGCGTGGAGCCATCAGGGGATTTATGCTTTCCCAATCCGATC	1350
QY	1419	ACTAAGCTAAACACCACTGATGATCAAGACCTTTTACAGACTGTGTCCCTCGAA	1478
Db	1351	ACAGCGTTCAACACTATGCCAGTTGATTAAGAGATTATTTACAGACTGTGGGCTTTTGAA	1410
QY	1479	TGCTCTTCTCTTTGTGACTACAGAAATGACATGATATGCCAGTAATTTGTGATGACATT	1538
Db	1411	TGCTCTTCTTTGTGTACTCTATAAATGATATGATACCCAGCAAAATTTGTGACATATTA	1470
QY	1539	CTGTATGCTCCAGCAGGACTTGGATATATTCAGCTATATGCGACATTATGCCCTGACATC	1598
Db	1471	CCATACCGCCCTCAGAGGACTGTGGGATGCTACAGCTATTTGGCAGCTGTGCTTGGCTGTC	1530
QY	1599	ATATTTAATTAATTAATGACAGATTCACCTTTTGGCATCAACGTCATCAACGCTGTTC	1658
Db	1531	GTGTTCAGATTTATTTATGACAGCTTCACCTTTGGATTAAAGTACCTTCAAGCTGTGTTT	1500
QY	1659	ATCCCCAGCATGCGCATTTGGAGGATCGCAGAGAGATTGTGGGATTTGCGGTGAGCAG	1718
Db	1591	ATCCCAAGCATGAGGAATTTGGTGCATAGCAGCGCGGATTTGTGGCATTCAGGTGACAA	1650
QY	1719	CTTGCTACATATCACCAACACTGTGTTATCTTTAAGAGTGTGTGAGAGTGGGCGTAT	1778
Db	1651	CTGCTTATATATCATATGATGACTGTGTTCAATTTCAAGAGATGATGGAAGTGGGAGCTGAC	1710
QY	1779	TGCATTTACACCTGAGCCCTTTTGGCATGTTGTGCTGCTGCATCTTAAAGTGGTGCACA	1838
Db	1711	TGTATACCTCTGGGCTATATGCTATGTTGTGTGCTGCTGCATGCTTTGTGATGACC	1770
QY	1839	AGATGACTGTCTCCCTGTGCTTATTTGTTTGTGACCTTACTGAGGCTTGGCATATAT	1898
Db	1771	CGGATGACAGCTCTCTCTTGATGACATAGATTTTGTGAGCTAATACGGGGGCTCGAATACATT	1830
QY	1899	GTTCCTCTTTATGCTGACATGATCAGTAATATGGTTGTGAGATGCTTTGGCAGGGA	1958
Db	1831	GTCCCCCTTATGGCAGCAGTGAATACCACTAATGTGGGATGCTTTTGGAAAGGAA	1890
QY	1959	GGCATTTATGAGACACATCGGATTAAATGATACCTTTCTTGATGCAAAAGAA	2018
Db	1891	GGATATATATAACTCATATACGCGCTGATGATATTCATTTTGGATGCCAAGAGAA	1950
QY	2019	TTTCACTATACCAACCGGCTGTGCTGATGATGAGACCCGCAAGGAATGATCTCCCTTA	2078
Db	1951	TTTCACTATACCACTCTAGCTGTGTATGATGAGCCCAAGAGAAACGATCTCTCATTG	2010
QY	2079	GCTGTCTGACAGACATATATGACATGATATATGAAACATGATTAATGAACC	2138
Db	2011	GCTGTCTTACTCAAGACGATATGACTGTGTATGATGTTGAAAGCTATATCAATGACACC	2070
QY	2139	AGCTACATGGAATTTCTCTGTATATATGTCAAAAGATCTCAGAGATTATGTGGATTTGCC	2198
Db	2071	AGCTACATGGAATTTCTCTGTATATATGTCAAAAGATCTCAGAGACTTGTGTGGATTTGCT	2130
QY	2199	CTCAGAGACACTGACAAATTTGCAATAGAACTGTCAGAGAAAAACAAGAGATATGCTT	2258
Db	2131	CTCAGAGAAATTTGACATTTAGCCATTTGAAATATGCAAGAAAAACAAGATGATATGTT	2190

Query Match	Best Local Similarity	Score	DB	Length
Matches 1705; Conservative	73.6%	0	No. 6.5e-223;	Mismatches 604; Indels 9; Gaps 2;
236	ACGACCTCATTTTACAAATGACAAATGAGGAGCATTT--AACGTTTACACATTTACT	292		
57	ACGATCTAATCAACGCGATGTCAACGCGGGGGGGGCTCCACGACGCTCCACCGCTGCT	116		
293	GGATCTTTTGATGTAACCAATTCACGCTGTGGTGTATCATATATGATATTTCCATTACTATGA	352		
117	GGACCTTCCATAGAGGAGGCCCATCCCTGGGTGGGAGCCATGACTCTTCAACACATGCA	176		
353	TTGGCTGGGAGAAAATGTAAAGACAGAAAAGCATAGACGATCAACAGCAAAAAGAA	412		
177	CTGGGTCGCTGAGAGGTCAAGACCGCGAGAGACACCGGAAGATCAATAGTAAGAAAA	236		
413	AGATTCACCATGGGAAATGACAAAAGTTTGTATCATGCGGTGTCAGGATGGCTAGTAGT	472		
237	GGAGTGGCATGGGAGTTCCACCAAAACCTGTACGACGCTGTGGCTGGCTGGGTGGT	296		
473	AACACTTAACAGAGATTTGGCATCAGGGGCACTGGCGGATTAATGACATTTGCTGGCATAT	532		
297	GACGCTCACTGGCTTTGGCATCAGTGTCTTTGGCTGGCTGATTTACATTTGCTGCTGATTTG	356		
533	CATGACTACCTAAAGAAGGCGATTTGCCCTTAGTGTGCTTTGGTGTACAAACAGCAAGCTG	592		
357	GATGACGACCTGAAGGAGGGGCGTGTGTCTGAGGCGCTTGTGGTTCAACCGAGCAGTGT	416		
593	CTGTTGGGGATCTAATGAAACACATTTGAAGAGAGGATTAATGTCCACGTTGGAAAC	652		
417	CTGGGAGCGTCAATGAGACCCATCTTCGTGAAGGAGAACAGTCTCCATGTAAGAGAG	476		
653	ATGGCAAAATTAATCATAGTCAAGCAGAGGCTCTGGTCTTATATCATGACATCAAT	712		
477	CTGGGCTAGCTAATATCTGGGGCAGGCTGAGGGCCCGGCTGCTGATCATGAACTATTT	536		
713	AATGTATCTCTTGGGCGCTTGAATTTGCCCTTTCGTCAGATTTCCCTGGTAAGGATTT	772		
537	CATGATCACTAATGAGGCTGTGCTCTTGGCTCTCTGCTGACATTTGTCTGGTTAAGGT	596		
773	TGCTTCATATGCTGTGCTCTGGAATTCGAGATTTAAACTATTTTAAGTGATTCAT	832		
597	TGCGCATATGACCTGGGCTCAGGATTCGAGAAATCAAGACCATCTGATGGGTTCAAT	656		
833	CATCAGAGTACTTCTGGAATAAGGACTTATGATTTAAACCATCAATCATAGCTGGG	892		
657	CATCGGGGCTATCTGGGCAAGTGACCTTATATATCAAAACCTCACTCTGCTGCTGGC	716		
893	TGTGGCATCAGCTTGAATTTAGAAAAAGAGTCCCTGGTATCATTTGGCTGTTGCTG	952		
717	TGTGGCGTGGGCGCTGAGACCTTGGGAAAGAGGGCCCTGTGTCACGTGGCTCTGCTG	776		
953	CGGAATATCTTTTCTCATCTCTTTTCCAAAGTATAGCAACAAGCAAGCTATAAAAAAGGA	1012		
777	TGGGAACATCTTCTCATCTCTTCTCCCAATGACGAAGAAGCAAGGCCAAGAAACAGA	836		
1013	GGTCTATACACTCTGCTCAGCTGACGGGTTCTGTAGCTTTTGGTGGACCAATTTGAGG	1072		
837	GGTCTCTCTGCGCCGCTGAGCTGCGGGGTGTCTGTAGCTTTTGGAGACCAATCGGGGG	896		
1073	AGTTCTTTTGAAGCTGGAAGAGTTAGCTATTTATTTTCTCTCAAACTTATGAGATC	1132		

Oy	1133	ATTTTTTCCTCTTATGAGCTGCAATTTGTTTGGAGTCCATCAATCAATTTGTTGAAACG	1192
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Oy	1253	TTTTATTTCTTAGGGATATTTGGAGGGCTTTGGGAGGCTTTTTCATTTAGGGCAAAAT	1312
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Oy	1313	TGCCCTGTGTCGACGCAAGTCCACGAATTTGGAAAGTATCCCGTTCGGAAGTCAT	1372
Db	1137	CGCCGTGGTCCGGGGGCAAGTCGACACGTTTGGCAGATACCGGTTGTTGAGGTGAT	1196
Oy	1373	TATTTTGCACCACTTATCTGCTGATAGCTTCCCTATTCATACACTAGCTAAACAC	1432
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Oy	1433	CAGTGAATGTATCAAAAGCTTTTTCACAGCTGTGTCCCTCGAATCCTCTCTCTTG	1492
Db	1257	CAGGAGCTGTATAAAGAGCTGTTTACACGACATCGGATCCGCTGAGTCTTCCGACCTTG	1316
Oy	1493	TGACTACAGAAATGATCATGAATGCCAGTAAATTTGTGATGACATTTCTGATGTCAGC	1552
Db	1317	TCAGTACGCGAGCCAGATGAAAGCGCACCAAAAGCTTCTCTGTA-----TGACACAGCCGCG	1370
Oy	1553	AGGCATTTGGAATATATTCACCTATATGGGAGATATCCGGGACATCATTTAAAAATCAT	1612
Db	1371	GGGGCCGGGCTCTACTCGGCACTGTGCGCACTGTGCTCTGGGGCTCATCTTTAAATATCAT	1430
Oy	1613	AATGACATATTCATTTTGGCATCAAGGTTTCCATCAGGCTTGTTCATCCCGACATGCG	1672
Db	1431	CATGACATATATTCATTTGGACTTGAAGTACCGTCCGGGTGTTCATCCCGACATGCG	1490
Oy	1673	CATTGGAGCATATCCAGAGAAATTTGGGGATTTGGGTGGAGCAGCTTGCTACTATCA	1732
Db	1491	CATTGGGGCGATCCGGGGGAGATGTGCGCACTGCGCAATGGAGCGCTGCAATATATCA	1550
Oy	1733	CCACAGCTGTTTTATCTTTTAAAGAGTGTGAGTGGGGGCTGTATTCATTACACCTGG	1792
Db	1551	CCACAGCTGGTTCCTGTTTCAAGAGTGTGTGCGAGGTGGGAGCTGACTGCATCCAGG	1610
Oy	1793	CCTTTATGCACTGGTGTGCTCTCTCATGCTTTAGTGGTGTGACAAAGATGACTGTC	1852
Db	1611	GCTCTATGTCAATGTGTGGACTCCACCGTCCCTGGGTGGAGTGCATCTGATGACCGTCC	1670
Oy	1853	CCCTGGTGTATTTGTTTTTAAAGCTTCTGGAAGGCTTGGAAATATTTGTTCCCTTAAGGC	1912
Db	1671	CCCTGCTATCATGCTGTTCAGACTGACCGGCGGGCTGGAGTACATCGTCCCTCATATGGC	1730
Oy	1913	TGCAGTCATGACCAAGTAAATGGGTTGGAATGCTTTGGCAGAGGAAGCAATTTATGAAGC	1972
Db	1731	CGCCGTATGACACGAAATGGGTGGGCGACGCAATTTGGCCGAGGGAAATCTACGAGGC	1790
Oy	1973	ACACATCCGATTAATATGATACCTCTTCTTGATGCAAAAGAGATTCATCTACCTACCAC	2032
Db	1791	CCACATCCGCTGAACGATACCCCTTCCCTGATTTCAATGAAGGAGGTTCACGCAACACCAC	1850
Oy	2033	CTTGGCTGTGACGTTATGAGACCTTGGAGGAATGATCCTCCCTAGTGTGTCGACACA	2092
Db	1851	GCTGGCCGGGAGTGTAGGGCCCGAGCGCAACGACCCGCGTTGGCAGTGTCTACGCA	1910
Oy	2093	GGACAAATATGACAGTGGATGATATAGAAAACATGATTAATGAACACAGCTTCAATTCGAT	2152
Db	1911	GGAGAGCACTACTGTGGAGAGCTGACGCGCATTTCAATGAAGAACATGATTAATGCTTT	1970
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ORIGIN				
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Db	2151	CTCCATTCCTGGAGACATGAGGCCCTTTCACCTCTCACTATGACACACACCCCATGAGATGTGGT	2210	
QY	2393	GGATATTTTCCGAAGCTCGGACTGAGCAGTGCCTTGTAACTCAATGAGGCGCTCTCT	2452	
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QY	2453	TGGCATTTTAAACAAAAAAGATATCTCCGCGATTTGGCCCGAGGCGGCAACCAAGACACC	2512	
Db	2271	TGCTATTATACAAAAAAGATATCTCTTGTCATAGGCTCAAAATGCAAAATCAGGATTC	2330	
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RESULT 13				
LOCUS	RNCHCHAMP	2244 bp	mRNA	linear
DEFINITION	R.norvegicus mRNA for putative chloride channel.			ROD 29-FEB-1996
ACCESSION	Z36944			
VERSION	Z36944.1	GI:535931		
KEYWORDS	chloride channel.			
SOURCE	Rattus norvegicus.			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
REFERENCE	1 (bases 1 to 2244)			
AUTHORS	Jentsch, T.J., Guenther, W., Pusch, M. and Schwappach, B.			
TITLE	Properties of voltage-gated chloride channels of the CLC gene family			
JOURNAL	J. Physiol.	482, 19-25	(1995)	
REFERENCE	2 (bases 1 to 2244)			
AUTHORS	Schwappach, B.			
TITLE	Direct Submission			
JOURNAL	Submitted (03-SEP-1994)			
FEATURES	Neurobiologie, Martinistr. 52, Hamburg, 20246, Germany			
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Db	2222	CTGAATCCATCATTTTAAAT	2242																			
RESULT 14																						
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DEFINITION	H.sapiens voltage-gated chloride ion channel CLCN5.																					
ACCESSION	X91906																					
VERSION	X91906.1	GI:1067131																				
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SOURCE	Homo sapiens.																					
ORGANISM	Homo sapiens.																					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.																					
AUTHORS	1 (bases 1 to 3173) Fisher,S.E., Van Bakel,I., Lloyd,S.E., Pearce,S.H., Thakker,R.V. and Craig,I.W.																					
TITLE	Cloning and characterization of CLCN5, the human kidney chloride channel gene implicated in Dent disease (an X-linked hereditary nephrolithiasis)																					
JOURNAL	Genomics 29 (3), 598-606 (1995)																					
MEDLINE	96121370																					
PUBMED	8575751																					
REFERENCE	2 (bases 1 to 3173) Craig,I.W.																					
AUTHORS	Direct Submission																					
TITLE	Submitted (30-AUG-1995) I.W. Craig, University of Oxford, Genetics Laboratory, Dept. of Biochemistry, South Parks Road, Oxford OX1 3QU, UK																					
JOURNAL	3 (bases 1 to 3173) Lloyd,S.E., Pearce,S.H.S., Fisher,S.E., Steinmeyer,K., Schwappach,B., Scheinman,S.J., Harding,B., Bolino,A., Devoto,M., Goodyer,P., Rigden,S.P.A., Wrong,O., Jentsch,T.J., Craig,I.W. and Thakker,R.V.																					
MEDLINE	A common molecular basis for three inherited kidney stone diseases Nature 379 (6564), 445-449 (1996)																					
PUBMED	96158876																					
COMMENT	8559248																					
FEATURES	Related sequences X81836 and 256277.																					
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